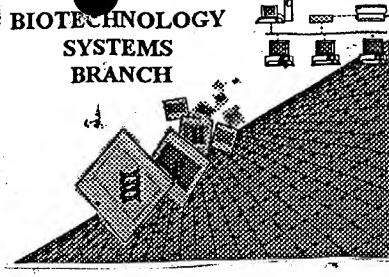


12D13

## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



1655  
H2K  
PP

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/345,761A  
Source: 1600  
Date Processed by STIC: 11/28/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

## Raw Sequence Listing Error Summary

ERROR DETECTED    SUGGESTED CORRECTION    SERIAL NUMBER: 09|345,761A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1  Wrapped Nucleic  
     Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2  Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3  Misaligned Amino  
     Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4  Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5  Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6  PatentIn 2.0  
     "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7  Skipped Sequences  
     (OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(ii) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8  Skipped Sequences  
     (NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000

9  Use of n's or Xaa's  
     (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10  Invalid <213>  
     Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11  Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12  PatentIn 2.0  
     "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1600

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/345,761A

DATE: 11/28/2001  
 TIME: 13:24:17

Input Set : A:\Q54969 - 09-345,761 Sequence Listing.txt  
 Output Set: N:\CRF3\11212001\I345761A.raw

3 <110> APPLICANT: ISHIGURO, Takahiko  
 4 SAITOH, Juichi  
 5 ISHIZUKA, Tetsuya  
 7 <120> TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID  
 9 <130> FILE REFERENCE: Q54969  
 11 <140> CURRENT APPLICATION NUMBER: US 09/345,761A  
 12 <141> CURRENT FILING DATE: 1999-07-01  
 14 <150> PRIOR APPLICATION NUMBER: JP 10-186434  
 15 <151> PRIOR FILING DATE: 1998-07-01  
 17 <160> NUMBER OF SEQ ID NOS: 7  
 19 <170> SOFTWARE: PatentIn version 3.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 50  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: synthetic construct  
 26 <400> SEQUENCE: 1  
 27 atttaggtga cactatagaa tacaacactc caccatagat cactccctg 50  
 30 <210> SEQ ID NO: 2  
 31 <211> LENGTH: 19  
 32 <212> TYPE: DNA  
 33 <213> ORGANISM: synthetic construct  
 35 <400> SEQUENCE: 2  
 36 actcgcaagg acccttatca 19  
 39 <210> SEQ ID NO: 3  
 40 <211> LENGTH: 11  
 41 <212> TYPE: DNA  
 42 <213> ORGANISM: synthetic construct  
 44 <400> SEQUENCE: 3  
 45 gtcggcccca a 11  
 48 <210> SEQ ID NO: 4  
 49 <211> LENGTH: 133  
 50 <212> TYPE: RNA  
 51 <213> ORGANISM: synthetic construct  
 53 <400> SEQUENCE: 4  
 54 ggaaagccu gcaugccugc aggucgacuc uagaggaucc ccggguaccc agcucgaaau 60  
 56 ccuugggggc gacacuccac cauagauac ucccuguga ggaacuacug ucuucacgca 120  
 58 gaaagcguu agc 133  
 61 <210> SEQ ID NO: 5  
 62 <211> LENGTH: 13  
 63 <212> TYPE: DNA  
 64 <213> ORGANISM: synthetic construct  
 66 <400> SEQUENCE: 5  
 67 ctccgcgggg ctg 13  
 70 <210> SEQ ID NO: 6  
 71 <211> LENGTH: 315  
 72 <212> TYPE: DNA  
 73 <213> ORGANISM: Synthetic Construct

Does Not Comply  
 Corrected Diskette Needed

invalid, see error summary sheet,  
 Item 10

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/345,761A

DATE: 11/28/2001

TIME: 13:24:17

Input Set : A:\Q54969 - 09-345,761 Sequence Listing.txt  
Output Set: N:\CRF3\11212001\I345761A.raw

75 <400> SEQUENCE: 6  
76 atttaggtga cactatagaa tacaacactc caccatagat cactccctg tgaggaacta 60  
78 ctgttettcac gcagaaaagcg tctagccatg gcgttagtat gagtgtcggt cagctccag 120  
80 gaccccccctt cccgggagag ccatagtggt ctgcggacc ggtgagtaca ccggaaattgc 180  
82 caggacgacc gggtccttcc ttggatcaac ccgctcaatg cctggagatt tggcgtgcc 240  
84 cccgcgagac tgctagccga gtatgtttgg gtcgcgaaag gccttgtgtt actgcctgat 300  
86 agggtgcttg cgagt 315  
89 <210> SEQ ID NO: 7  
90 <211> LENGTH: 298  
91 <212> TYPE: RNA  
92 <213> ORGANISM: Synthetic Construct  
94 <400> SEQUENCE:  
95 gaauacaaca cuccaccaua gaucacuccc cugugaggaa cuacugucuu cacgcagaaa 60  
97 ggcgcuagcc auggcguuag uaugaguguc gugcagccuc caggacccccc ccuuccggga 120  
99 gagccauagu ggucugcgga accggugagu acaccggaaau ugccaggacg accggguccu 180  
101 uucuuggaau aaccgcuca augccuggag auuugggcgu gcccccgcgaa gacugcuagc 240  
103 cgaguagugu ugggcgcgaa aaggccuugu gguacugccu gauagggugc uugcgagu 298

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/345,761A

DATE: 11/28/2001

TIME: 13:24:18

Input Set : A:\Q54969 - 09-345,761 Sequence Listing.txt  
Output Set: N:\CRF3\11212001\I345761A.raw